



urn:lsid:zoobank.org:pub:BC39D736-FFFC-481D-B5FA-6CB84EA4E7AA

A new cryptic species of *Cnemaspis* Strauch, 1887 (Squamata: Gekkonidae), in the *C. littoralis* complex, from Anakkal, Palakkad, Kerala, India

^{1,*†}Amit Sayyed, ^{2,†}Vivek Philip Cyriac, and ³Raveendan Dileepkumar

¹Wildlife Protection and Research Society, Maharashtra, INDIA ²IISER-TVM Centre for Research and Education in Ecology and Evolution (ICREEE), School of Biology, Indian Institute of Science Education and Research, Thiruvananthapuram, Kerala 695551, INDIA ³YIPB Department of Biotechnology, University of Kerala, INDIA

Abstract.—A new cryptic species of the gekkonid genus *Cnemaspis* is described from the Central Western Ghats of Kerala, India. *Cnemaspis palakkadensis* sp. nov. is a small-sized (snout-vent length less than 35 mm) *Cnemaspis* in the *littoralis* clade. Although the new species superficially resembles *C. littoralis*, it shows moderate levels of genetic divergence in the 16S rRNA gene, and can be differentiated from all other Indian congeners by a suite of distinct morphological characters: dorsal scales homogenous, small, smooth; absence of conical or spine-like tubercles on flanks; ventral scales smooth, imbricate; dorsal scales of limbs smooth; 15 or 16 femoral pores on each side separated by 14 poreless scales; lamellae under fourth digit of manus 12–15 and pes 14–17; absence of whorls of pointed tubercles on tail; median subcaudals enlarged, imbricate, smooth. The species is found in an ignored low-lying forest habitat in parts of the Anakkal reserve forest in Kerala.

Keywords. Asia, description, dwarf gecko, mountains, Reptilia, southern Western Ghats

Citation: Sayyed A, Cyriac VP, Dileepkumar R. 2020. A new cryptic species of *Cnemaspis* Strauch, 1887 (Squamata: Gekkonidae), in the *C. littoralis* complex, from Anakkal, Palakkad, Kerala, India. *Amphibian & Reptile Conservation* 14(3) [Taxonomy Section]: 31–45 (e251).

Copyright: © 2020 Sayyed et al. This is an open access article distributed under the terms of the Creative Commons Attribution License [Attribution 4.0 International (CC BY 4.0): <https://creativecommons.org/licenses/by/4.0/>], which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited. The official and authorized publication credit sources, which will be duly enforced, are as follows: official journal title *Amphibian & Reptile Conservation*; official journal website: amphibian-reptile-conservation.org.

Accepted: 15 July 2020; Published: 8 September 2020

Introduction

The genus *Cnemaspis* Strauch, 1887 is among the most speciose of the Old World gekkonid genera, with at least 168 known species, ranking as the second most diverse gecko genus in the world after *Cyrtodactylus* (Uetz et al. 2020). Although large-scale molecular phylogenetic analyses have recently shown the genus to be polyphyletic (Gamble et al. 2012; Pyron et al. 2013; Zhang and Wiens 2016), there has been limited effort to resolve these issues, probably due to the lack of widespread sampling, specifically in the Indian region. With 48 species in mainland India, *Cnemaspis* represents the largest group of geckos in the country, with a large majority of the species restricted to the Western Ghats.

The Western Ghats, a long north-south orientated mountain chain extending from Gujarat in the north (21.00°N) to the southern tip of peninsular India in Tamil Nadu (08.25°N), is one of the 36 global biodiversity hotspots (Myers et al. 2000). Its historical isolation from

neighboring regions, complex topography, and humid tropical to subtropical climate have resulted in a high level of generic endemism, which is specifically accentuated in many amphibians and reptiles (Vijayakumar et al. 2014; Cyriac and Kodandaramaiah 2017). Widespread exploration in the higher reaches of the Western Ghats has rapidly increased the number of reptile and amphibian species in India (e.g., Zacharyah et al. 2011; Biju et al. 2014; Vijayakumar et al. 2014; Zacharyah et al. 2016; Sayyed et al. 2018; Chaitanya et al. 2019). However, recent surveys in the low-lying regions of the Western Ghats and several isolated hillocks in peninsular India are revealing a great amount of undocumented lizard diversity, especially among members of the genus *Cnemaspis* (Khandaker et al. 2019; Agarwal et al. 2020; Cyriac et al. 2020). In light of this, field surveys were conducted in the lowland forests bordering the Palghat gap in Kerala and Tamil Nadu, the largest geographical break in the long Western Ghats chain of mountains. These explorations revealed a new undescribed species

Correspondence. ^{1,*}amitsayyedsatara@gmail.com, ²vivek.cyriac@gmail.com, ³dileepkamukumpuzha@gmail.com, [†]Authors contributed equally to this work.

which resembles the widespread *C. littoralis* (Jerdon) and is described here based on its genetic distinctiveness and a suite of distinct morphological characters.

Materials and Methods

Field sampling and specimens. Field surveys were conducted during May 2019, in parts of Anakkal, Palakkad District, Kerala, India. Specific sampling locations were chosen based on previous observations. All adult specimens were collected by hand, photographed in life, and then euthanized using halothane. Thigh muscles were collected as tissue samples for further genetic analysis, after which specimens were fixed in 4% formaldehyde for ~24 hours, washed in water, and transferred to 70% ethanol for long-term storage. Scalation and other morphological characters were recorded using a Lensei stereo microscope. The materials referred to in this study are deposited in the collection of the Bombay Natural History Society (BNHS), Mumbai, and were collected under the permits issued by the Kerala Forest and Wildlife Department (permits to RD, numbers WL10-41691/2014 and 94/2009).

Phylogenetic analysis. Total genomic DNA was extracted from the tissue samples using protocols as per Sayyed et al. (2016). The 16S rRNA mitochondrial gene was amplified using the primers designed by Palumbi et al. (1991) following standard 3-step PCR protocols (Palumbi 1996). The amplicons were then Sanger sequenced using the primers. The resulting sequences were manually checked for sequencing artifacts, and then added to the 16S rRNA sequence matrix generated by Cyriac et al. (2020) for the Indian *Cnemaspis*. However, *C. nilagirica* was removed from the matrix generated by Cyriac et al. (2020), since we found that the sample used was contaminated. The sequences were aligned using the MAFFT algorithm (Katoh and Standley 2013). The pair-wise uncorrected *p*-distances between and within species for the 16S rRNA gene were then calculated after removing all ambiguous positions for each sequence pair using MEGAX (Kumar et al. 2018). For the downstream phylogenetic analysis, multiple sequences of the same species were removed, except for the two sequences of *C. littoralis*. The best-fit substitution model was determined using PartitionFinder 2 (Lanfear et al. 2016) on the final 596 bp dataset and then a Maximum Likelihood analysis was performed using IQ-TREE (Nguyen et al. 2015) under the GTR+I+G substitution model with 1,000 standard bootstrap replicates. The MAFFT alignment, Partition Finder analysis, and Maximum Likelihood analysis were carried out using the phylogenetic workflow implemented in the PhyloSuite platform (Zhang et al. 2020). Following Cyriac et al. (2020), the tree was rooted by including three species of *Lygodactylus* and three species of *Phelsuma* as outgroups for the phylogenetic reconstruction (see Appendix 1).

Morphological and meristic data. For the specimens listed in Appendix 2, the following measurements were taken using a Yamayo digimatic calliper, a Mitutoyo 500, or a Tesacalip 64 (to the nearest 0.1 mm): snout-vent length (SVL), from tip of snout to anterior edge of cloacal opening; trunk length (TL), distance from axilla to groin measured from posterior edge of the forelimb insertion to the anterior edge of the hind limb insertion; trunk width (TW), maximum width of body; tail length (TAL), from vent to tip of tail; tail width (TLW), measured at widest point of tail; head length (HL), distance from tip of snout to posterior edge of mandible; head width (HW), maximum width of head; head depth (HD), maximum depth of head, from occiput to underside of jaws; upper arm length (UAL), distance from axilla to elbow; forearm length (FAL), from base of palm to elbow; femur length (FEL), distance from groin to the knee; tibia length (TBL), knee to tarsus; toe length (TOL), distance from tip of toe to the nearest fork; palm length (PAL), distance between posterior-most margin of palm and tip of fourth digit; finger length (FL), distance from the tip of the finger to the nearest fork; eye to nares distance (E-N), distance between anterior-most point of eye and nostril; eye to snout distance (E-S), distance between anterior-most point of eye and tip of snout; eye to ear distance (E-E), distance from anterior edge of ear opening to posterior corner of eye; tympanum diameter (EL), maximum distance end-to-end (height) of ear opening; distance between nares (IN), right to left nare; orbital diameter (OD), greatest diameter of orbit; interorbital snout distance (IO), distance between orbit and snout on frontal bone.

Meristic data recorded for all specimens were number of supralabials (SupL) and infralabials (InfL) on left (L) and right (R) sides; number of interorbital scales (InO); number of postmentals (PoM); number of posterior postmentals (PoP), scales that are surrounded by the posterior-postmentals and between infralabials; number of supranasals (SuN), excluding the smaller scales between the larger supranasals; number of the postnasals (PoN), all scales posterior to the naris; number of supraciliaries (SuS); number of scales between eye and tympanum (BeT), from posterior-most point of the orbit to anterior-most point of the tympanum; number of canthal scales (CaS), number of scales from posterior-most point of naris to anterior-most point of the orbit; number of dorsal paravertebral scales (PvS), between pelvic and pectoral limb insertion points along a straight line immediately left of the vertebral column; number of mid-dorsal scales (MbS), from the center of mid-dorsal row diagonally towards the ventral scales; number of midventral scales (MvS), from the first scale posterior to the mental to the last scale anterior to the vent; number of mid-body scales (BIS), across the ventral between the lowest rows of dorsal scales; femoral pores (FPores), the number of femoral pores; lamellae under digits of manus (MLam) and pes (PLam) on right (R) side, counted from

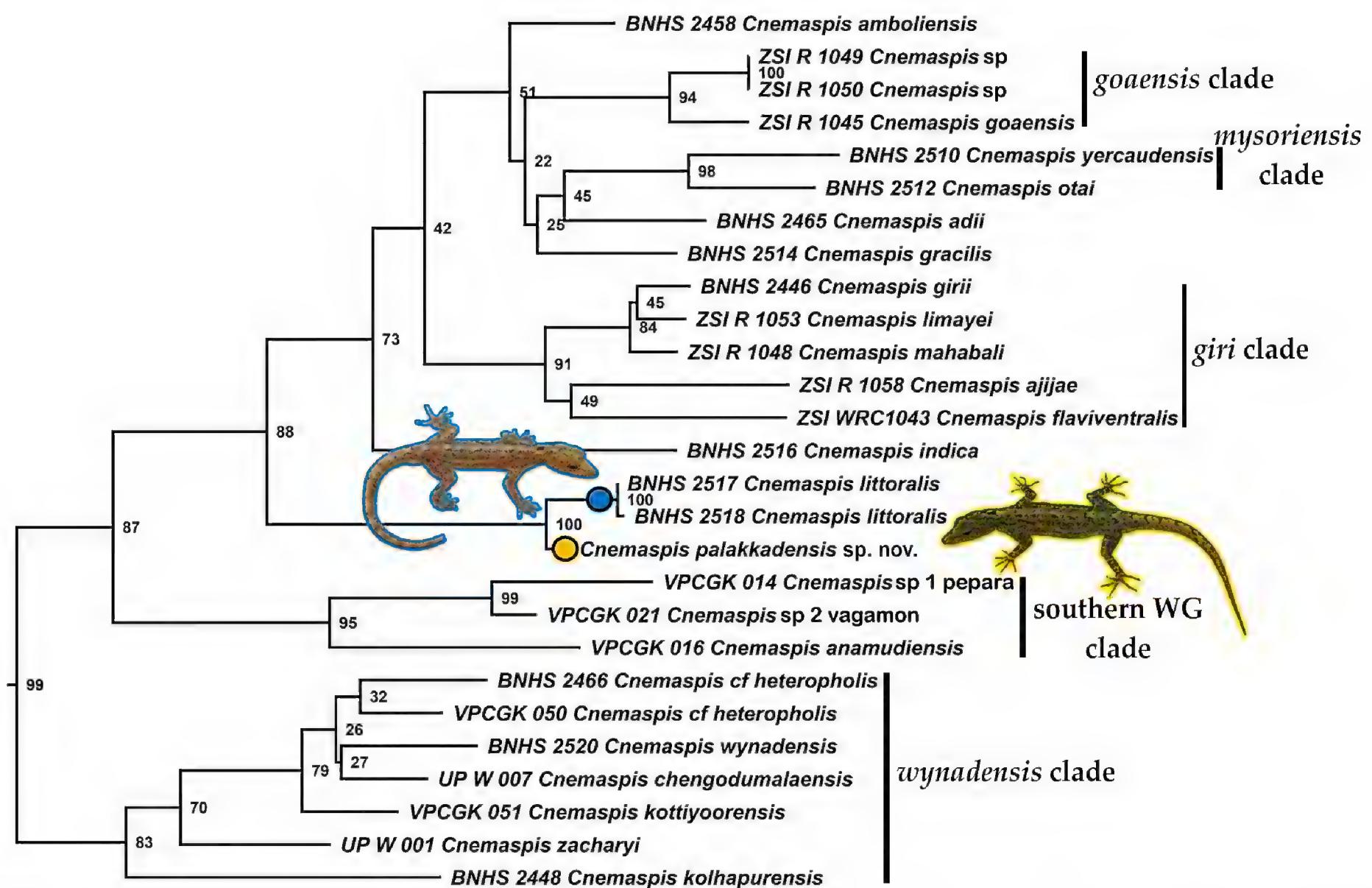


Fig. 1. 16S rRNA tree of the Indian *Cnemaspis* obtained from the Maximum Likelihood analysis in IQ-TREE. Node values indicate bootstrap support with values < 70 indicating low support, values between 70–90 indicating moderate support, and values > 90 indicating strong support. The blue and yellow circles represent the branches leading to *C. littoralis* and *C. palakkadensis* sp. nov., respectively, along with representative images of the two species indicated by their blue (*C. littoralis*) and yellow (*C. palakkadensis* sp. nov.) borders.

first proximal enlarged scansor greater than twice width of the largest palm scale, to distal-most lamella at tip of digits; and lamellae under fourth digit of pes (LampIV). For the geographical coordinates, altitude, and temperature readings, a Kestrel 4500 receiver was used. Opportunistic observations on the ecology of the species were also made during field work. Since the specimens from Palakkad most closely resembled *Cnemaspis littoralis*, specimens were compared with the neotype of *C. littoralis* and other associated material deposited at the Zoological Survey of India Western Ghats Regional Center (ZSI-WGRC), Kozhikode, India.

Morphometric analysis. The morphometric analysis was performed in R V. 3.5.2 (R Core Team 2016). A multivariate analysis was carried out on 25 morphometric variables. This analysis included only 25 variables for the analysis out of the 29 variables collected because some variables were unavailable for a few specimens due to missing tails or digits (see Table 3). A Principal Component Analysis (PCA) was performed on the 25 variables to identify the variables that contributed to the observed variation in the data. Plots were generated for the first and second, and the first and third principal components to visually examine the morphospace of

the new species and the morphologically similar *C. littoralis*.

Results

Phylogenetic Relationships

The topology recovered by the Maximum Likelihood analysis indicated well-supported deeper nodes but showed low support for many shallower nodes (Fig. 1). The topology was mostly consistent with the topology recovered by Sayyed et al. (2018) and Cyriac et al. (2010), except for the position of *Cnemaspis indica* where *C. indica* was sister to members of the *giri*, *gracilis*, *mysoriensis*, *goaensis*, and *amboliensis* clades. The new species was recovered as being sister to *C. littoralis* with very strong support (Fig. 1). The *littoralis* clade was sister to the (*indica* + (*giri* + (((*adii* + *mysoriensis*) + *gracilis*) + *goaensis*) + *amboliensis*)) clade. Uncorrected pairwise sequence divergence for the 16S rRNA gene indicated that the *littoralis* clade was deeply divergent from the rest of the species (sequence divergence > 10). However, there was only a moderate level of genetic divergence between *C. littoralis* and *C. palakkadensis* sp. nov., which ranged between 2.5–2.7%.

Table 1. Loadings obtained from the Principal Component Analysis of the 25 morphometric variables. Bold values indicate strong loading with correlation > 0.5.

Character	Description	PC1	PC2	PC3
SVL	Snout-vent length	-0.8278	-0.3045	-0.2238
TL	Axilla-groin distance	-0.8229	-0.2799	-0.2737
TW	Trunk width	-0.7241	-0.4259	-0.3070
OD	Eye diameter	0.6453	-0.6311	-0.0557
E-N	Eye-to-nasal distance	-0.9000	0.2800	0.0950
E-S	Snout length	-0.7350	-0.3478	-0.0852
E-E	Eye-to-ear distance	-0.3239	-0.5513	0.4186
IN	Inter-nasal distance	-0.9745	0.1924	-0.0163
EL	Horizontal diameter of ear opening	0.4675	-0.7923	-0.1568
HL	Head length	-0.6952	-0.5014	0.2935
HW	Head width	-0.8603	-0.3320	0.2034
HD	Head depth	-0.3677	-0.2852	0.5858
IO	Inter-orbital distance	-0.6162	-0.0902	-0.5711
UAL	Upper arm length	-0.4407	-0.7307	0.1714
FAL	Lower arm length	-0.6657	-0.4920	0.3509
PAL	Palm length	-0.7949	0.2111	-0.2336
FL1	Length of 1 st finger	0.5045	-0.5947	0.0675
FL3	Length of 3 rd finger	0.6421	-0.0028	0.3832
FL4	Length of 4 th finger	0.7575	-0.4670	0.0566
FL5	Length of 5 th finger	0.6749	-0.5265	-0.3075
FEL	Femur length	-0.9383	-0.2243	0.0515
TBL	Tibia length	-0.6979	-0.1892	0.2162
TOL1	Length of 1 st toe	0.7920	-0.5161	-0.0054
TOL2	Length of 2 nd toe	0.6670	-0.6226	-0.1914
TOL4	Length of 4 th toe	-0.4037	-0.5158	-0.4972
Eigenvalue		12.2328	5.0454	2.0250
Standard deviation		3.4976	2.2462	1.4230
Proportion of variance		0.4893	0.2018	0.0810
Cumulative proportion		0.4893	0.6911	0.7721

Morphometric Analysis

Principal Component Analysis indicated that the first three PCs explained 77.7% of the variation in morphology. PC1 explained ca. 48.9% of the variation and described a shorter, slender body form with a shorter head, shorter snout, larger eyes, and short limbs (Table 1). PC2 explained ca. 20.2% of the variation and is described mostly by smaller eyes, shorter eye-to-ear distance, smaller ear opening, and shorter forelimbs (Table 1). PC3 explained ca. 8.1% of the variation and described a less depressed head and narrower interorbital region (Table 1). Plots of PC1 with PC2 and PC1 with PC3 indicated considerable differences in the morphospace between the new species and *C. littoralis*, with the differences being along PC1 (Fig. 2A–B).

Systematics

Cnemaspis palakkadensis sp. nov.

Figs. 3–7; Tables 2–4.

urn:lsid:zoobank.org:act:4A854A91-206D-41E0-959E-5761F3040380

Holotype. BNHS 2790, an adult male, 32.2 mm SVL, from Anakkal (10°52'50"N, 76°39'23"E; ca. 140 m asl), Palakkad District, Kerala, south-western India (Fig. 1), collected by Amit Sayyed, 18 May 2019.

Paratype. BNHS 2791, an adult male, 31.5 mm SVL, and BNHS 2792, an adult female, 34.1 mm SVL; collected from same locality as holotype by Vivek Vaidyanathan and Abhijit Nale, 19 May 2019.

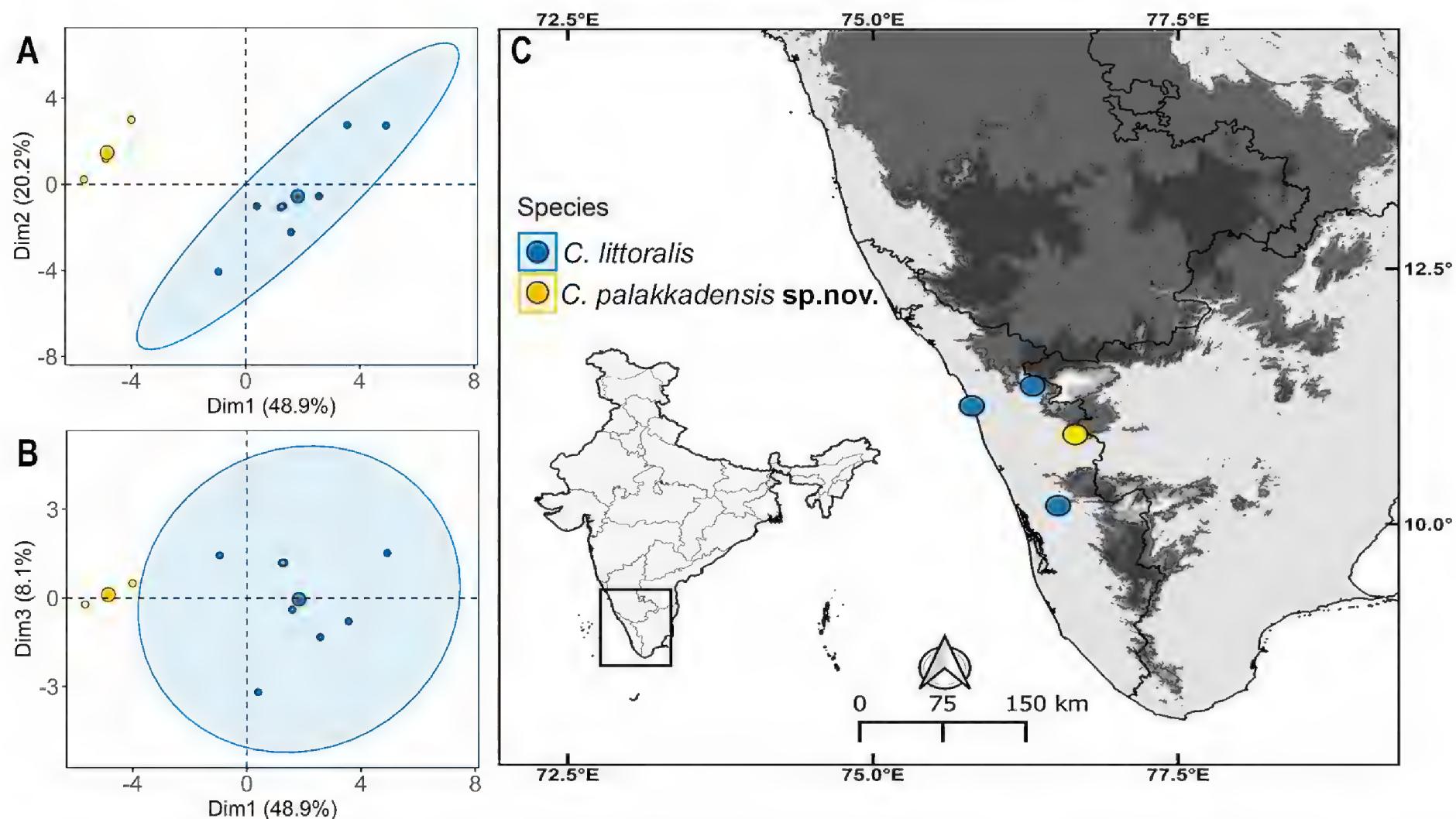


Fig. 2. Results of the morphometric analysis comparing the morphospace occupied by *Cnemaspis littoralis* and *C. palakkadensis* sp. nov. **(A)** Morphospace occupied by the two species as indicated by the first two dimensions (PC1 and PC2); **(B)** morphospace occupied by the two species as indicated by the first and third dimensions (PC1 and PC3); and **(C)** map showing the distributions of *C. littoralis* and *C. palakkadensis* sp. nov. The blue and yellow points in the morphospace and the map correspond to *C. littoralis* and *C. palakkadensis* sp. nov., respectively.

Diagnosis and comparison with Indian congeners. A small-sized *Cnemaspis*, SVL < 35 mm; dorsal pholidosis homogenous with small, smooth, granular scales in the vertebral and paravertebral regions; conical or spine-like tubercles absent on flank; ventral scales smooth, imbricate; males with 15–16 femoral pores on each thigh and no pre-cloacal pores; supralabials to angle of jaw 7–8, infralabials to angle of jaw 6–8; lamellae under fourth digit of manus 12–15, and pes 14–17; tail without whorls of enlarged tubercles; median subcaudals enlarged, imbricate, smooth, post cloacal spur absent in both sexes.

Cnemaspis palakkadensis sp. nov. can be distinguished from all other Indian congeners on the basis of the following differing or non-overlapping characters: Spine-like tubercles absent on flanks [versus spine-like tubercles present on flank in *C. amboliensis* Sayyed, Pyron, and Dileepkumar, *C. assamensis* Das and Sengupta, *C. anandani* Murthy, Nitesh, Sengupta, and Deepak, *C. flaviventralis* Sayyed, Pyron, and Dahanukar, *C. goaensis* Sharma, *C. gracilis* (Beddome), *C. jerdonii* (Theobald), *C. koynaensis* Khandekar, Thackery, and Agarwal, *C. monticola* Manamendra-Arachchi, Batuwita, and Pethiyagoda, *C. mysoriensis* (Jerdon), *C. monticola* Manamendra-Arachchi, Batuwita, and Pethiyagoda, *C. nilagirica* Manamendra-Arachchi, Batuwita, and Pethiyagoda, and *C. otai* Das and Bauer]. Dorsal scales on midbody homogenous [versus heterogeneous in *C. aaronbaueri* Sayyed, Grismer, Campbell, and

Dileepkumar, *C. agarwali* Khandekar, *C. ajijae* Sayyed, Pyron, and Dileepkumar, *C. amba* Khandekar, Thackery, and Agarwal, *C. amboliensis*, *C. anamudiensis* Cyriac, Johny, Umesh, and Palot, *C. anandani*, *C. andersonii* (Annandale), *C. australis* Manamendra-Arachchi, Batuwita, and Pethiyagoda, *C. avasabinae* Agarwal, Bauer, and Khandekar, *C. bangara* Agarwal, Thackeray, Pal, and Khandekar, *C. beddomei* (Theobald), *C. chengodumalaensis* Cyriac, Palot, and Deutiand Umesh, *C. flaviventralis*, *C. girii* Mirza, Pal, Bhosale, and Sanap, *C. goaensis*, *C. gracilis*, *C. graniticola* Agarwal, Thackeray, Pal, and Khandekar, *C. heteropholis* Bauer, *C. kottiyorensis* Cyriac and Umesh, *C. koynaensis*, *C. limayei* Sayyed, Pyron, and Dileepkumar, *C. maculicollis* Cyriac, Johny, Umesh, and Palot, *C. mahabali* Sayyed, Pyron, and Dileepkumar, *C. monticola* Manamendra-Arachchi, Batuwita, and Pethiyagoda, *C. nairi* Inger, Marx, and Koshy, 1984, *C. ornata* (Beddome), *C. shevaroyensis* Khandekar, Gaitonde and Agarwal, *C. sisparensis* (Theobald), *C. thackerayi* Khandekar, Gaitonde, and Agarwal, *C. wicksii* (Stoliczka), *C. yelagiriensis* Agarwal, Thackeray, Pal, and Khandekar, and *C. yercaudensis* Das and Bauer]. Presence of a series of 15–16 femoral pores on each side and the absence of pre-cloacal pores in males [versus absence of femoral pores in *C. aaronbaueri*, *C. anamudiensis*, *C. avasabinae*, *C. assamensis*, *C. beddomei*, *C. boiei* (Gray), *C. maculicollis*, *C. nairi*, and *C. ornata*; presence of both pre-cloacal and femoral pores in *C. adii*, *C.*

Table 2. Measurements (to the nearest 0.1 mm) of the type series of *Cnemaspis palakkadensis* sp. nov. Measurement abbreviations are defined in the text.

Measurement	Holotype		Paratypes	
	BNHS 2790	BNHS 2791	BNHS 2792	BNHS 2792
Sex	male	male	female	
SVL	32.2	31.5	34.0	
TL	15.6	14.6	16.7	
TW	6.4	5.2	6.8	
TAL	35.7	32.6	33.3	
TLW	3.4	2.7	2.8	
HL	8.9	8.7	9.1	
HW	5.2	5.1	5.2	
HD	3.3	3.3	3.5	
UAL	4.5	3.8	4.6	
FAL	5.5	5.3	5.6	
FEL	5.8	5.7	5.9	
TBL	5.9	5.9	6.0	
PAL	3.7	3.6	3.9	
E-N	4.0	4.0	4.2	
E-S	4.1	4.1	4.3	
E-E	2.5	2.5	2.5	
EL	0.3	0.2	0.3	
IN	1.6	1.6	1.6	
OD	1.2	1.2	1.2	
IO	3.3	3.2	3.4	

agarwali, *C. amboliensis*, *C. andersonii*, *C. australis*, *C. bangara*, *C. gracilis*, *C. goaensis*, *C. graniticola*, *C. mysoriensis*, *C. otai*, *C. shevaroyensis*, *C. thackerayi*, *C. wicksii*, *C. yelagiriensis*, and *C. yercaudensis*]; and from the following species by presence large number of femoral pores [versus < 10 femoral pores on each side in *C. ajijae*, *C. amba*, *C. anandani*, *C. chengodumalaensis*, *C. flaviventralis*, *C. girii*, *C. heteropholis*, *C. indica*, *C. jerdonii*, *C. kottiyorensis*, *C. koynaensis*, *C. limayei*, *C. mahabali*, *C. nilagirica*, *C. sisparensis*, *C. wynadensis*, and *C. zacharyi* Cyriac, Palot, and Deutiand Umesh; and a continuous series of precloacal-femoral pores in *C. kolhapurensis*]. Median subcaudals enlarged [versus small median subcaudals in *C. adii*, *C. ajijae*, *C. amba*, *C. andersonii*, *C. flaviventralis*, *C. girii*, *C. gracilis*, *C. koynaensis*, and *C. limayei*].

Cnemaspis palakkadensis sp. nov. could be confused with the morphologically similar *C. littoralis* (Jerdon), but can be distinguished by its longer trunk length (AG 46–49% of SVL versus AG 37–46% of SVL in *C. littoralis*); much smaller eyes (ED 13–14% of HL versus ED 16–21% of SVL in *C. littoralis*); absence of conical or spine-like tubercles on flanks (versus small spine-like tubercles present on flanks in *C. littoralis*); supralabials to angle of jaw 7–8 (versus 9–10 supralabials in *C. littoralis*); number of scales between eye and tympanum 18–19 (versus 17); mid-dorsal scales 54–57 (versus 52);

midventral scales 130–134 (versus 122); number of mid-body scales 32–38 (versus 26); absence of a small post-cloacal spur on both sides of the tail and absence of whorls of enlarged tubercles on the tail (versus a single post-cloacal spur present on each side of the tail and whorls of small but enlarged tubercles on the dorsal side of the tail in *C. littoralis*).

Description of holotype. An adult male of SVL 32.2 mm (Fig. 3A–B); head moderately short (HL 17.6% of SVL), narrow (HW 15.9% of SVL), flat (HD 59.4% of HL), distinct from neck; snout short (E-S 78.6% of HL), slightly curved laterally; scales on snout granular, smooth, larger than those on the forehead and interorbital region (Fig. 4A); eye small (OD 21.8% of HL); pupil rounded; 13 supraciliaries; 30 interorbital scales; ear opening small (EL 5.7% of HL), longer than broad; 18 scales between eye and tympanum. Rostral wider than long, partially divided by a deep median groove; nostrils small, bordered posteriorly by two small, granular, postnasal scales; single enlarged supranasal on each side separated by an elongated intermediate scale. Mental large, triangular, not pointed posteriorly, broader than long, bordered posteriorly by two postmentals and a single intermediate chin shield broadly separated the postmentals, eight scales surrounded posteriorly by the posterior postmentals, infralabials, and the mental;

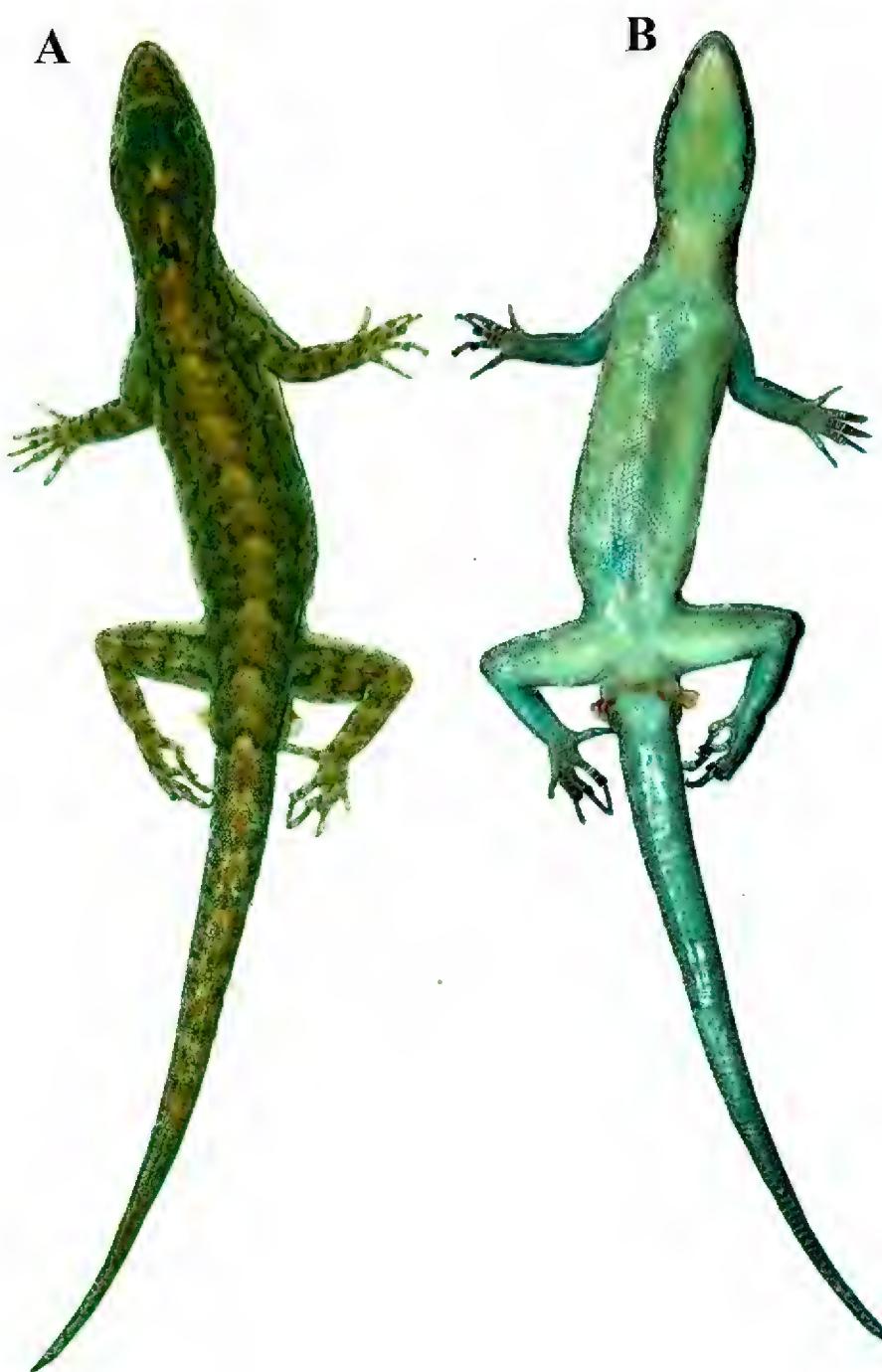


Fig. 3. Holotype (BNHS 2790) of *Cnemaspis palakkadensis* sp. nov. (A) Dorsal view and (B) ventral view of full-body. *Photos by Amit Sayyed.*

three smooth, large scales posteriorly surrounded by intermediate chin shield; gular scales granular, smooth, larger than those on throat (Fig. 4B). Seven supralabials to angle of jaw on each side, supralabial I largest, decreasing in size posteriorly; six infralabials to angle of jaw on each side, infralabial I largest, decreasing in size posteriorly (Fig. 4C).

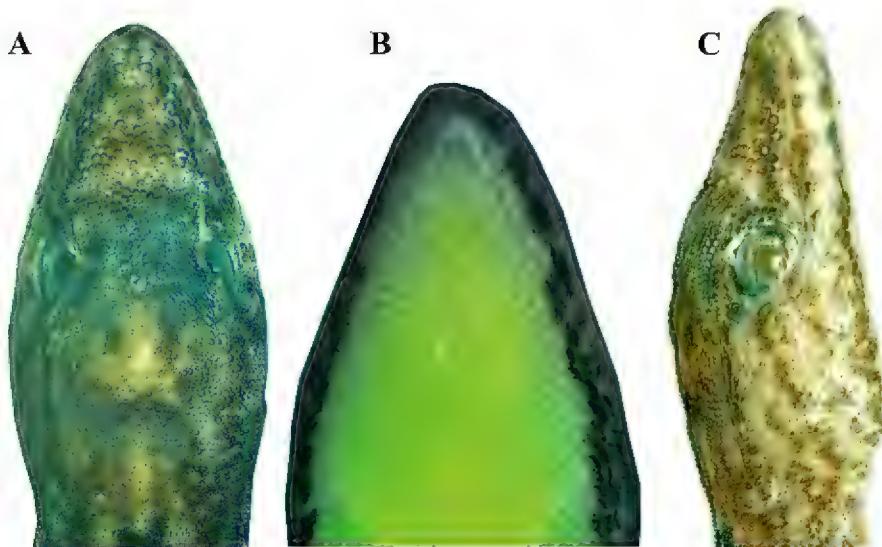


Fig. 4. Holotype (BNHS 2790) of *Cnemaspis palakkadensis* sp. nov. (A) Dorsal, (B) ventral, and (C) lateral views of the head. *Photos by Amit Sayyed.*

Body slender, short (TL 40%) without conical or spine-like tubercles on flanks (Fig. 5A, C). Dorsal scales of the body and flank homogenous, small, granular, smooth; scales on forehead, neck, and dorsal body equal in size; paravertebral scales 112; number of mid-dorsal scales 54; scales arranged in 33–35 longitudinal rows at midbody, number of midventral scales 131, smooth, imbricate, larger than dorsals (Fig. 5B). Fore and hind limbs relatively long, slender (FL 16.8%; TBL 16.4%); dorsal scales of brachium granular, smooth, larger than forearm; dorsal scales of forearm small, granular; ventral scales of brachium and forearm small, smooth; dorsal scales on palm, foot and fingers granular, smooth; scales on palmar and plantar surfaces smooth; subdigital lamellae entire, few fragmented; series of unpaired lamellae on basal portion of digits, separated from fragmented distal lamellae by a single large scale at the inflection; proximal lamellae series: 1-3-4-4-3 (right manus), 1-4-5-6-3 (right pes); distal lamellae series: 9-11-14-14-12 (right manus), 9-13-15-17-11 (right pes). Relative lengths of digits, fingers: IV (2.71 mm) > III (2.53 mm) > II (2.42 mm) > V (1.87 mm) > I (1.18 mm); toes: IV (3.68 mm) > III (3.16 mm) > II (1.99 mm) > V (1.75 mm) > I (0.85 mm) [Fig. 6A–B]. Femoral pores 15; 14 poreless scales between right and left femoral pore series; three rows of enlarged, roughly hexagonal scales above the femoral pores, larger than those on precloacal region; no precloacal pores; precloacal scales equal in size to the belly scales (Fig. 6C).

Tail long (TAL 111%), cylindrical, base swollen; post-cloacal spur absent on each side of lateral surface of hemipenal bulges at base of tail; dorsal scales of tail homogenous, smooth, granular, without enlarged, conical tubercles forming whorls, ventral scales imbricate, smooth; median subcaudals enlarged, smooth; those at the base are moderately smaller and imbricate (Fig. 6D–F).

Coloration in life (Fig. 6A–C). Male and female of the new species are the same in dorsal appearance. Dorsum of head mottled with brown and yellow; ventral side of head bright orange-yellow in males but white in females, bordered by a dark brown line up to the throat; nape with a small, black ocelli-like marking. Iris yellow with thin dark yellow line bordering pupil; pupil circular, black; supraciliaries yellow; supralabials and infralabials yellow. Dorsum of the body and limbs dull grey with brown and pale yellowish mottling; vertebral region pale yellow with 6–7 dark-edged lighter markings. Tail dull brown dorsally, with irregular faded yellow spots. Ventral side of body and tail white.

Coloration in preservative. Dorsum of the body and limbs with brown which turns into dark brown and pale yellow mottling and into grey; ventral side of body and tail greyish white; ventral side of head in males grey with slight yellowish tinge.

Table 3. Meristic data for the type series of *Cnemaspis palakkadensis* sp. nov. The symbol “?” indicates a broken finger, and “–” indicates pores not present.

Character	Holotype (BNHS 2790)	Paratype (BNHS 2791)	Paratype (BNHS 2792)
Sex	male	male	female
SupL R/L	7/7	8/8	8/8
InfL R/L	6/6	8/8	8/7
SuS	13	13	13
InO	30	32	31
BeT	18	18	19
PoN	2	2	2
PoM	2	2	2
PoP	8	10	8
SuN	1	1	1
CaS	14	15	14
PvS	112	109	113
MbS	54	54	57
MvS	131	130	134
BIS	33–35	32–34	35–38
FPores	15/15	16/16	–
MLam R	9-11-14-14-12	7-10-12-12-11	9-?-13-15-13
PLam R	9-13-15-17-11	7-12-?-14-13	9-14-16-17-15

Variation of the type series (Tables 1–3). The SVL of adult specimens in the type series of *Cnemaspis palakkadensis* sp. nov. ($n = 3$) ranges from 31.5 to 34.1 mm; number of posterior postmentals, 8–10; scales between eye and tympanum, 18–19; number of interorbitals, 30–32; number of canthal scales, 14–15; number of dorsal paravertebral scales, 109–113; number of mid-dorsal scales, 54–57; number of midventral scales from mental to cloaca, 130–134; number of mid-body scales across belly, 32–38; lamellae under fourth digit of manus (MLamIV) and pes (PLamIV), 12–15 and 14–17, respectively. Male and female paratypes match the holotype in overall coloration, except for the coloration on the throat.

Etymology. The specific epithet *palakkadensis* refers to the Palakkad district, from which the type series was collected.

Suggested Common Name. Palakkad Dwarf Gecko.

Distribution. At present, the new species is only known from the type locality in Anakkal reserve forest ($10^{\circ}52'50''\text{N}$ $76^{\circ}39'23''\text{E}$) in Palakkad District of Kerala state (Fig. 1C), which is a low-land moist deciduous to riparian forest at an elevation of 84–170 m asl on the northern border of the Palghat gap, a ca. 30-km gap separating the central and southern Western Ghats. However, it is possible that the range of this species may extend to other low-land forests in the Palakkad region of Kerala and Coimbatore of Tamil Nadu.

Natural history. The species is found in low-land moist deciduous to semi-evergreen forest habitat of Palakkad hills of the Central Western Ghats. The climate of the region is moist and humid, and the area is rich in natural forest. All the specimens were found active during the day on the trunks, branches, and exposed roots of large trees around small streams (Fig. 8A–B), suggesting that this species is arboreal and diurnal. Single eggs or pairs of eggs were observed in several tree holes during the field survey (Fig. 7D). Two eggs that were collected measured 5.1×4.9 mm and 5.2×5.0 mm. The types were found sympatrically with *Ophiophagus hannah* (Cantor), *Trimeresurus gramineus* (Shaw), *Naja naja* (Linnaeus), *Hypnale hypnale* (Merrem), *Ahaetulla nasuta* Lacepede, *Amphiesma stolatum* (Linnaeus), *Lycodon aulicus* (Linnaeus), *Dendrelaphis tristis* (Daudin), *Cnemaspis gracilis*, *Cnemaspis* sp., *Psammophilus dorsalis* (Gray), and *Psammophilus* sp. (Stoliczka).

Discussion

The phylogenetic analysis recovered a topology mostly concordant with previous studies employing the 16S rRNA gene (Sayyed et al. 2018; Cyriac et al. 2020), even after the removal of *Cnemaspis nilagirica* from the sequence matrix. However, there was a difference in the phylogenetic placement of *Cnemaspis indica*. While this analysis recovered moderate support for a sister relationship between *C. indica* and members of the *giri*, *gracilis*, *mysoriensis*, *goaensis*, and *amboliensis* clades (Fig. 1), Sayyed et al. (2018) and Cyriac et al. (2020)

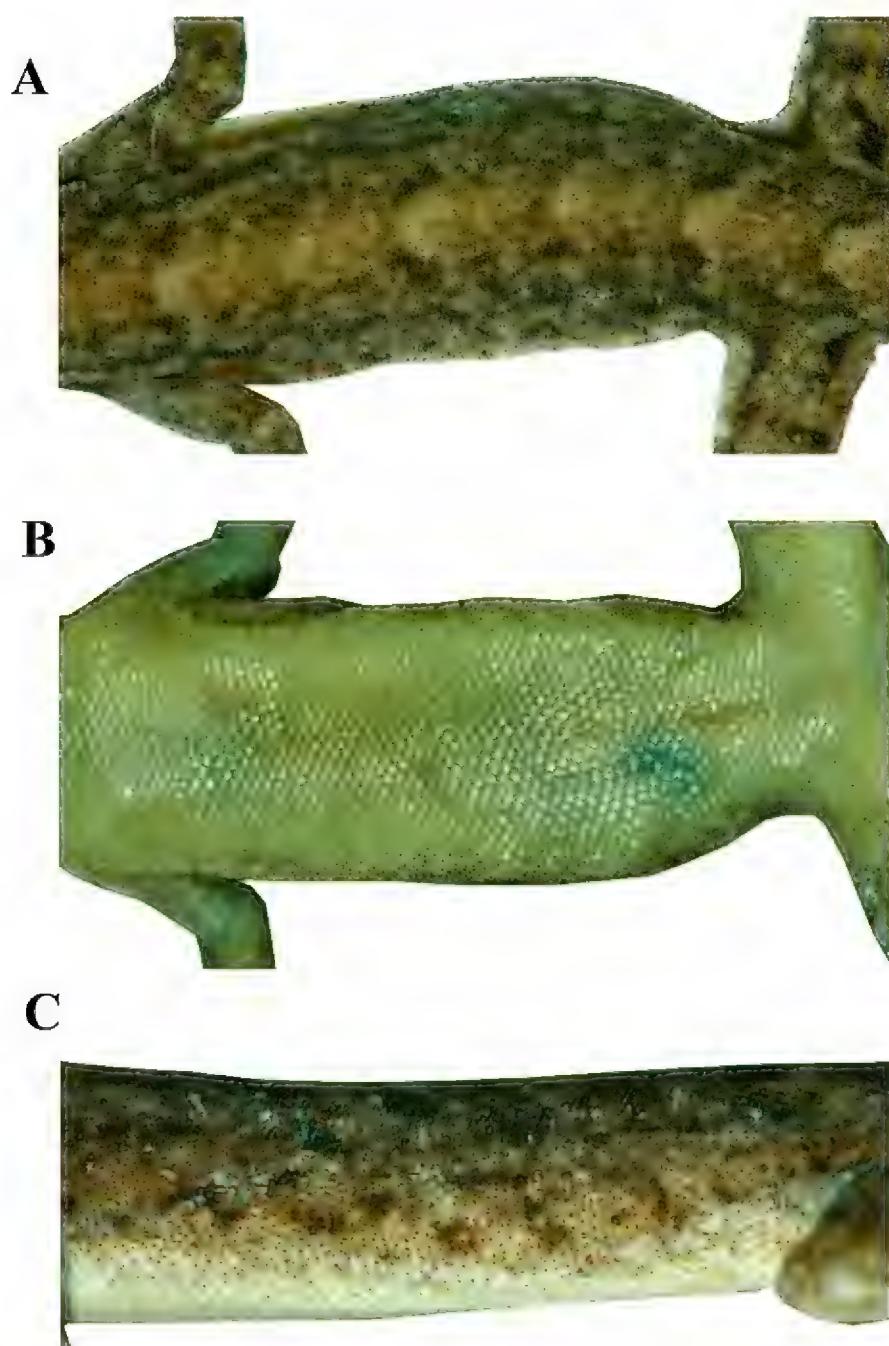


Fig. 5. Holotype (BNHS 2790) of *Cnemaspis palakkadensis* sp. nov. (A) Dorsal pholidosis at midbody, (B) ventral scales at midbody, (C) scales on lateral surface of trunk. *Photos by Amit Sayyed.*

recovered a sister relationship between *C. indica* and members of the *gracilis*, *mysoriensis*, *goaensis*, and *amboliensis* clades, albeit with very low support. Such discordance could be due to the removal of *C. nilagirica* from the analysis or the differences in our analytical approach. Nonetheless, our analysis indicates slightly improved support values for deeper nodes compared to earlier 16S rRNA trees.

The analysis clearly indicated that *Cnemaspis palakkadensis* sp. nov. was sister to *C. littoralis*, and showed moderate levels genetic divergence (2.5–2.7%) from the latter. Although genetic divergences of 2–4% are considered low for the 16S rRNA gene, morphologically distinct species have been shown to exhibit shallow genetic divergence (ca. 1%) for the 16S rRNA gene (Shanker et al. 2017). The specimens described here as *C. palakkadensis* sp. nov. occupy a distinct morphospace compared to *C. littoralis*, despite the superficial morphological resemblance and shallow genetic divergence with *C. littoralis*. Further, the genetic divergence between *C. palakkadensis* sp. nov. and *C. littoralis* was greater than the average intraspecific genetic divergence estimated for 16 *Cnemaspis* species based on the 16S rRNA gene of only $0.4 \pm 0.42\%$, with the maximum intraspecific genetic divergence recorded

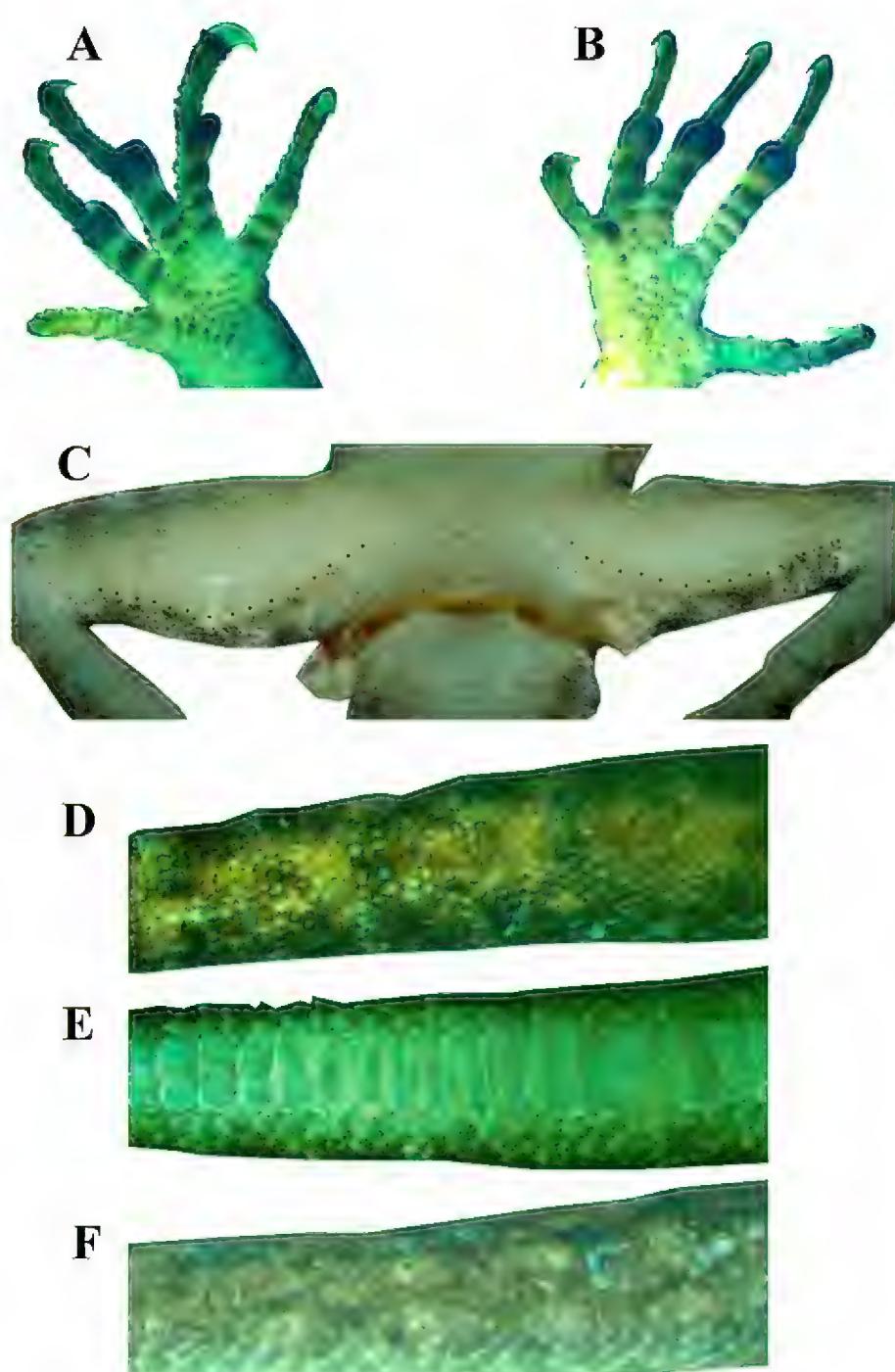


Fig. 6. Holotype (BNHS 2790) of *Cnemaspis palakkadensis* sp. nov. (A) Lamellae on manus, (B) lamellae on pes, (C) femoral pores, (D) dorsal scalation of tail, (E) subcaudals, (F) lateral side of tail. *Photos by Amit Sayyed.*

being 1.7% (see Appendix 3). The two species are also morphologically distinct and can be distinguished based on several non-overlapping diagnostic characters.

Interestingly, *C. palakkadensis* sp. nov. was found in low-land moist deciduous to semi-evergreen forests in the northern border of the Palghat gap. This gap forms a major dispersal barrier and biogeographic divide to many groups of animals which are distributed on the higher reaches of the Western Ghats (Robin et al. 2010; Van Bocxlaer et al. 2012; Vijayakumar et al. 2014). However, our understanding of what biogeographic barriers influence the distribution of low-land habitat-specialist species remains poor, mostly due to the lack of systematic exploration of low-lying regions. The discovery of *C. palakkadensis* sp. nov. from the low-land forests in the Palghat gap further highlight the presence of unknown diversity within the species *C. littoralis*, which is thought to have a wide distribution in the littoral regions of Kerala (Cyriac and Umesh 2013). However, widespread systematic explorations in these low-land forests will be necessary to determine the distributional range of this species. Cyriac and Umesh (2013) designated a neotype for *C. littoralis* based on specimens



Fig. 7. Color in life of *Cnemaspis palakkadensis* sp. nov. (A) Holotype male (BNHS 2790), (B) paratype female (BNHS 2792), (C) holotype male (BNHS 2790) showing the coloration of throat, (D) egg. Photos by Amit Sayyed.

collected from Chaliyam coast in Kozhikode, Kerala, and reported additional specimens from Narayamkulam (= Chengodumala) in Kozhikode district, Nellikuth in Malapuram district, and Kapprikad in Ernakulam district of Kerala. They also reported observations of *C. littoralis* from Kannur, Thrissur, Palakkad, Ernakulam, and Thiruvananthapuram in Kerala. However, given the possibility of cryptic species within this group, the true distribution of *C. littoralis* will need further evaluation.

Recent and current explorations in the high and low mountains of the Western Ghats of India have led to the discovery of several unique species of the genus *Cnemaspis*. Although most of them are from isolated humid forest (Giri et al. 2009b; Srinivasulu et al. 2015; Cyriac et al. 2018; Khandekar et al. 2019a; Sayyed et al. 2019), ongoing studies are showing that *Cnemaspis* can also be found in drier regions. With the discovery of *C. palakkadensis* sp. nov., the number of *Cnemaspis* species in the Indian mainland increases to 43, yet the true diversity within this group is clearly far from being totally uncovered. Recent studies have also hinted at the presence of cryptic diversity within the south Asian *Cnemaspis* (Agarwal et al. 2017; Cyriac et al. 2020). The current study further calls attention to cryptic diversity within the Western Ghats and adjacent low-lying regions. Thus, widespread fine-scale sampling will be critical for uncovering species richness and distributional patterns within the group.

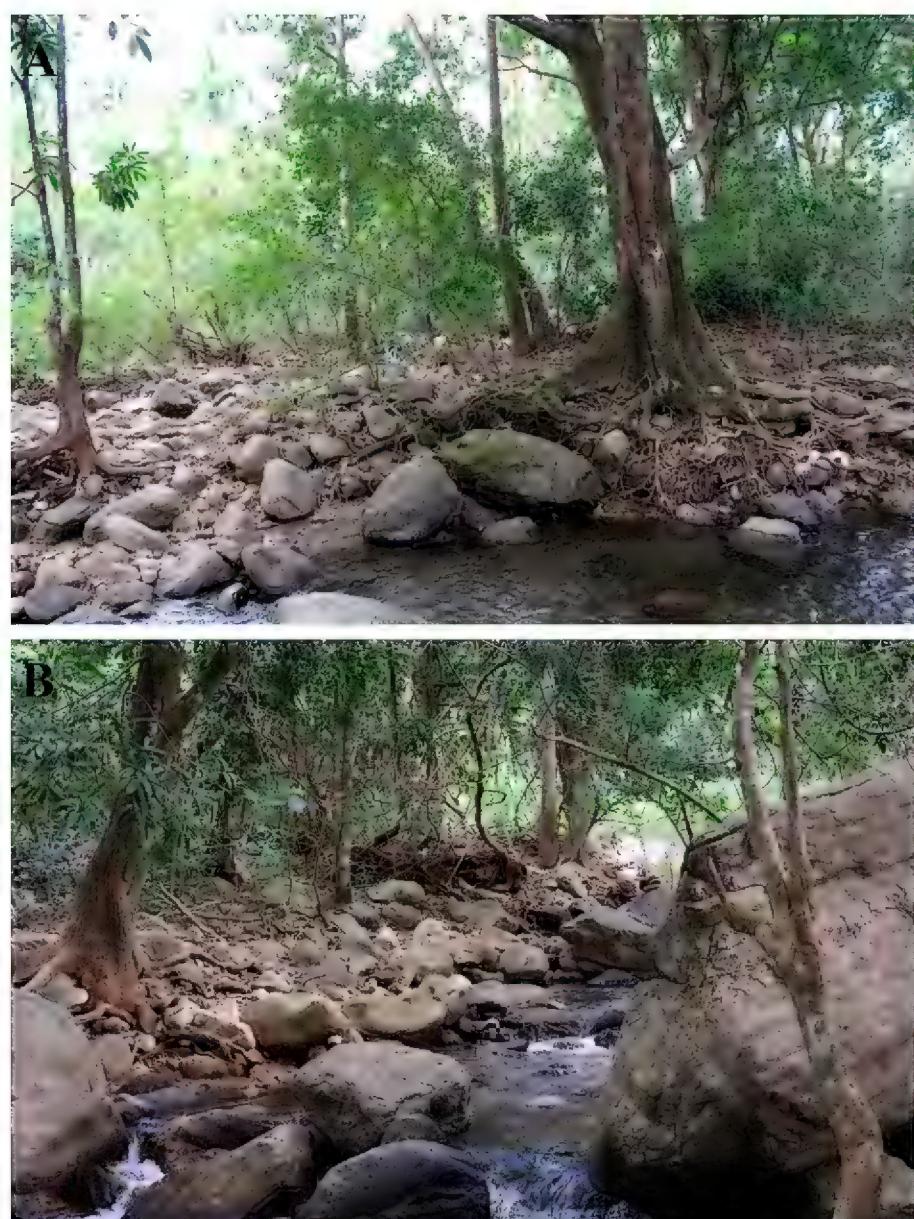


Fig. 8. Habitat of *Cnemaspis palakkadensis* sp. nov. Photos by Amit Sayyed.

Acknowledgments.—The authors are thankful to the Forest Departments of Kerala for issuing collecting permits, and for their support during field surveys. Deepak Apte (Director) and Rahul Khot (museum curator) of the Bombay Natural History Society, Mumbai, provided access to specimens and registration of the type specimens. We also thank Vithoba Hegde, Umesh P.K., Vivek Vidyanathan, Abhijit Nale, Kiran Ahire, Vikas Jagtap, Mahesh Bandgar, Ayaan Sayyed, and Masum Sayyed for help during fieldwork and for their support.

Literature Cited

Bauer AM. 2002. Two new species of *Cnemaspis* (Reptilia: Squamata: Gekkonidae) from Gund, Uttara Kannada, India. *Mitteilungen aus dem Hamburgischen Zoologischen Museum und Institut* 99: 155–167.

Biju SD, Garg S, Gururaja KV, Shouche Y, Walujkar SA. 2014. DNA barcoding reveals unprecedented diversity in Dancing Frogs of India (Micrixalidae, *Micrixalus*): a taxonomic revision with description of 14 new species. *Ceylon Journal of Science (Biological Sciences)* 43(1): 37–123.

Chaitanya R, Giri VB, Deepak V, Datta-Roy A, Murthy BHCK, Karanth P. 2019. Diversification in the mountains: a generic reappraisal of the Western Ghats endemic gecko genus *Dravidogecko* Smith, 1933 (Squamata: Gekkonidae) with descriptions of six new species. *Zootaxa* 4688: 1–56.

Cyriac VP, Umesh PK. 2013. Current status of *Cnemaspis littoralis* (Jerdon, 1853) (Sauria: Gekkonidae) with designation of a neotype. *Taprobanica: the Journal of Asian Biodiversity* 5: 36–43.

Cyriac VP, Umesh PK. 2014. Description of a new ground-dwelling *Cnemaspis* Strauch, 1887 (Squamata: Gekkonidae), from Kerala, allied to *C. wynadensis* (Beddome, 1870). *Russian Journal of Herpetology* 21(3): 187–194.

Cyriac VP, Kodandaramaiah U. 2017. Paleoclimate determines diversification patterns in the fossorial snake family Uropeltidae Cuvier, 1829. *Molecular Phylogenetics and Evolution* 116: 97–107.

Cyriac VP, Johny A, Umesh PK, Palot MJ. 2018. Description of two new species of *Cnemaspis* Strauch, 1887 (Squamata: Gekkonidae) from the Western Ghats of Kerala, India. *Zootaxa* 4459: 85–100.

Cyriac VP, Palot MJ, Deuti K, Umesh PK. 2020. A preliminary 16S rRNA phylogeny of the Indian *Cnemaspis* Strauch, 1887 (Squamata: Gekkonidae) with the description of two new cryptic species from the *C. wynadensis* clade. *Vertebrate Zoology* 70(2): 171–193.

Das I, Bauer AM. 2000. Two new species of *Cnemaspis* (Sauria: Gekkonidae) from Tamil Nadu, southern India. *Russian Journal of Herpetology* 7(1): 17–28.

Das I, Sengupta S. 2000. A new species of *Cnemaspis* (Sauria: Gekkonidae) from Assam, northeastern India. *Journal of South Asian Natural History* 5(1): 17–23.

Gamble T, Greenbaum E, Jackman TR, Russell AP, Bauer AM. 2012. Repeated origin and loss of adhesive toepads in geckos. *PLoS ONE* 7(6): e39429.

Giri VB, Agarwal I, Bauer AM. 2009a. Designation of a neotype for *Cnemaspis mysoriensis* (Jerdon 1853) (Sauria: Gekkonidae), with a re-description and notes on its distribution and habitat. *Russian Journal of Herpetology* 16: 256–264.

Giri VB, Bauer AM, Gaikwad KS. 2009b. A new ground-dwelling species of *Cnemaspis* Strauch (Squamata: Gekkonidae) from the northern Western Ghats, Maharashtra, India. *Zootaxa* 2164: 49–60.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution* 30(4): 772–780.

Khandekar A. 2019. A new species of rock-dwelling *Cnemaspis* Strauch, 1887 (Squamata: Gekkonidae) from Tamil Nadu, southern India. *Zootaxa* 4571: 383–397.

Khandekar A, Thackery T, Agarwal I. 2019a. Two more new species of *Cnemaspis* Strauch, 1887 (Squamata: Gekkonidae) from the northern Western Ghats, Maharashtra, India. *Zootaxa* 4656: 43–70.

Khandekar A, Gaitonde N, Agarwal I. 2019b. Two new *Cnemaspis* Strauch, 1887 (Squamata: Gekkonidae) from the Shevaroy massif, Tamil Nadu, India, with a preliminary ND2 phylogeny of Indian *Cnemaspis*. *Zootaxa* 4609: 68–100.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. *Molecular Biology and Evolution* 35(6): 1,547–1,549.

Lanfear R, Frandsen PB, Wright AM, Senfeld T, Calcott B. 2017. PartitionFinder 2: new methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. *Molecular Biology and Evolution* 34(3): 772–773.

Manamendra-Arachchi K, Batuwita S, Pethiyagoda R. 2007. A taxonomic revision of the Sri Lankan day-geckos (Reptilia: Gekkonidae: *Cnemaspis*), with descriptions of new species from Sri Lanka and southern India. *Zeylanica* 7: 9–122.

Mirza ZA. 2018. A new cryptic species of ground-dwelling *Hemidactylus* (Squamata: Gekkonidae) from southern India. *Phylomedusa* 17: 169–180.

Mirza ZA, Pal S, Bhosale HS, Sanap RV. 2014. A new species of gecko of the genus *Cnemaspis* Strauch, 1887 from the Western Ghats, India. *Zootaxa* 3815: 494–506.

Mukherjee D, Bhupathy S, Nixon AMA. 2005. A new species of day gecko (Squamata, Gekkonidae, *Cnemaspis*) from the Anaikatti Hills, Western Ghats, Tamil Nadu, India. *Current Science* 89: 1,326–1,328.

Murthy BHC, Nitesh A, Sengupta S, Deepak P. 2019. A new species of day gecko of the genus *Cnemaspis*

Strauch, 1887 (Squamata: Gekkonidae) from the Nilgiri Hills, Tamil Nadu, India. *Records of the Zoological Survey of India* 119(3): 211–226.

Myers N, Mittermeier RA, Mittermeier CG, Da Fonseca GA, Kent J. 2000. Biodiversity hotspots for conservation priorities. *Nature* 403: 853–858.

Nguyen LT, Schmidt HA, Von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution* 32(1): 268–274.

Palumbi SR. 1996. PCR and molecular systematics. *Molecular Systematics* 2: 205–247.

Palumbi SR, Martin A, Romano S, McMillan WO, Stice L, Grabowski G. 1991. *The Simple Fool's Guide to PCR, Version 2.0*. University of Hawaii, Honolulu, Hawaii, USA. 45 p.

Pyron RA, Burbrink FT, Wiens JJ. 2013. A phylogeny and revised classification of Squamata, including 4,161 species of lizards and snakes. *BMC Evolutionary Biology* 13(1): 1–54.

R Core Team. 2016. R: a language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.

Robin VV, Sinha A, Ramakrishnan U. 2010. Ancient geographical gaps and paleo-climate shape the phylogeography of an endemic bird in the sky islands of southern India. *PLoS ONE* 5(10): e13321.

Sayyed A, Pyron RA, Dahanukar N. 2016. *Cnemaspis flaviventralis*, a new species of gecko (Squamata: Gekkonidae) from the Western Ghats of Maharashtra, India. *Journal of Threatened Taxa* 8: 9,619–9,629.

Sayyed A, Pyron RA, Dileepkumar R. 2018. Four new species of the genus *Cnemaspis* Strauch, 1887 (Sauria: Gekkonidae) from the northern Western Ghats, India. *Amphibian & Reptile Conservation* 12(2) [General Section]: 1–29 (e157).

Sayyed A, Grismer LL, Campbell PD, Dileepkumar R. 2019. Description of a cryptic new species of *Cnemaspis* Strauch, 1887 (Squamata: Gekkonidae) from the Western Ghats of Kerala State of India. *Zootaxa* 4656: 501–514.

Shanker K, Vijayakumar SP, Ganeshiah KN. 2017. Unpacking the species conundrum: philosophy, practice, and a way forward. *Journal of Genetics* 96(3): 413–430.

Srinivasulu C, Kumar GC, Srinivasulu B. 2015. A new species of *Cnemaspis* (Sauria: Gekkonidae) from Northern Karnataka, India. *Zootaxa* 3947: 85–98.

Uetz P, Hošek J. 2019. The Reptile Database. Available: <http://www.reptile-database.org> [Accessed: 5 January 2020].

Van Bocxlaer I, Biju SD, Willaert B, Giri VB, Shouche YS, Bossuyt F. 2012. Mountain-associated clade endemism in an ancient frog family (Nyctibatrachidae) on the Indian subcontinent. *Molecular Phylogenetics and Evolution* 62(3): 839–847.

Vijayakumar SP, Dinesh KP, Prabhu MV, Shanker K. 2014. Lineage delimitation and description of nine new species of bush frogs (Anura: *Raorchestes*, Rhacophoridae) from the Western Ghats Escarpment. *Zootaxa* 3893(4): 451–488.

Vijayakumar SP, Menezes RC, Jayarajan A, Shanker K. 2016. Glaciations, gradients, and geography: multiple drivers of diversification of bush frogs in the Western Ghats Escarpment. *Proceedings of the Royal Society B: Biological Sciences* 283(1836): 20161011.

Zachariah A, Dinesh KP, Kunhikrishnan E, Das S, Raju DV, Radhakrishnan C, Palot MJ, Kalesh S. 2011. Nine new species of frogs of the genus *Raorchestes* (Amphibia: Anura: Rhacophoridae) from southern Western Ghats, India. *Biosystematica* 5: 25–48.

Zachariah A, Cyriac VP, Chandramohan B, Ansil BR, Mathew JK, Raju DV, Abraham RK. 2016. Two new species of *Raorchestes* (Anura: Rhacophoridae) from the Silent Valley National Park in the Nilgiri Hills of the Western Ghats, India. *Salamandra* 52(2): 63–76.

Zhang D, Gao F, Jakovlić I, Zou H, Zhang J, Li WX, Wang GT. 2020. PhyloSuite: an integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. *Molecular Ecology Resources* 20(1): 348–355.

Zheng Y, Wiens JJ. 2016. Combining phylogenomic and supermatrix approaches, and a time-calibrated phylogeny for squamate reptiles (lizards and snakes) based on 52 genes and 4,162 species. *Molecular Phylogenetics and Evolution* 94: 537–547.



Amit Sayyed is a herpetologist, and the founder and director of the Wildlife Protection and Research Society, India. Amit is working on the faunal diversity and conservation of reptiles, and his main interests have been in the taxonomy of snakes, geckos, and frogs. He has published several papers on natural history and faunal diversity, and thus far he has described eight new species. Amit is the author of three books: *Amazing Creatures of the Earth (Snakes of Maharashtra, Goa and Karnataka)*, *Butterflies and Spiders of The Western Ghats*, and *Dangerous Bite and First Aid*. His Ph.D. focused on wildlife conservation, and he plans to pursue further studies on the phylogenetic systematics, taxonomy, and natural history of the Indian species of the genus *Cnemaspis*.



Vivek Cyriac is an evolutionary ecologist from India with broad interests in the ecological and evolutionary mechanisms that generate biodiversity patterns. His work is centered around understanding how environmental factors and biotic interactions influence species diversification and create macro-evolutionary patterns. Vivek uses reptiles and amphibians as model systems to explore diverse questions in ecology, evolution, and behavior. Thus far, he has predominantly worked on fossorial uropeltid snakes and geckos of the genus *Cnemaspis*.



Raveendan Dileepkumar is currently a Principal Investigator under the Young Investigator's Program in Biotechnology in the Centre for Venom Informatics, University of Kerala, India. He is also co-investigating projects in the area of venomics supported by KSCSTE, Government of Kerala. His research broadly encompasses the venomics, venom gland transcriptomics, and genomics of venomous snakes; with ongoing projects centered on understanding the venom composition of venomous species in the animal kingdom. His publications, including book chapters, have focused on snake taxonomy, venomics, and venom applications in medical technologies.

A new *Cnemaspis* species from India

Appendix 1. GenBank accession number and voucher information for Indian *Cnemaspis* and outgroups used in the phylogenetic analysis. The line highlighted in bold indicates a new sequence generated for *C. palakkadensis* sp. nov. * indicates accession number of *C. kottiyoorensis* which was misprinted as MT217042 in Cyriac et al. (2020).

No	Species	Locality	Voucher	16s rRNA
1	<i>Cnemaspis mahabali</i>	Pune, Maharashtra	ZSI/R/1048	KX753643
2	<i>Cnemaspis amboliensis</i>	Sindhudurg, Maharashtra	BNHS 2458	MH174358
3	<i>Cnemaspis ajijae</i>	Satara, Maharashtra	ZSI WRC R/1058	KX753653
4	<i>Cnemaspis limayei</i>	Sindhudurg, Maharashtra	ZSI WRC R/1053	KX753647
5	<i>Cnemaspis yercaudensis</i>	Salem, Tamil Nadu	BNHS 2510	MH174360
6	<i>Cnemaspis otai</i>	Vellore, Tamil Nadu	BNHS 2512	MH174362
7	<i>Cnemaspis gracilis</i>	Palakkad, Kerala	BNHS 2514	MH174370
8	<i>Cnemaspis indica</i>	Nilgiris, Tamil Nadu	BNHS 2516	MH174366
9	<i>Cnemaspis littoralis</i>	Kozhikode, Kerala	BNHS 2517	MH174367
10	<i>Cnemaspis littoralis</i>	Kozhikode, Kerala	BNHS 2518	MH174368
11	<i>Cnemaspis kottiyoorensis</i>	Kannur, Kerala	BNHS 2519	MH174363
12	<i>Cnemaspis wynadensis</i>	Wayanad, Kerala	BNHS 2520	MH174364
13	<i>Cnemaspis goaensis</i>	Goa	ZSI WRC R/1045	KX269826
14	<i>Cnemaspis flaviventralis</i>	Sindhudurg, Maharashtra	ZSI WRC R/1043	KX269820
15	<i>Cnemaspis girii</i>	Satara, Maharashtra	BNHS 2446	KX269824
16	<i>Cnemaspis kolhapurensis</i>	Sindhudurg, Maharashtra	BNHS 2448	KX269822
17	<i>Cnemaspis heteropholis</i>	Shimoga, Karnataka	BNHS 2466	KX753660
18	<i>Cnemaspis adii</i>	Ballari, Karnataka	BNHS 2465	KX753655
19	<i>Cnemaspis goaensis</i>	Goa	ZSI WRC R/1044	KX269825
20	<i>Cnemaspis zacharyi</i>	Lakkadi, Wayanad, Kerala	BNHS 2735	MT217042
		Chengodumala, Kozhikode, Kerala		
21	<i>Cnemaspis chengodumalaensis</i>		BNHS 2741	MT217043
22	<i>Cnemaspis</i> sp. (Pepara)	Pepara WLS, Trivandrum, Kerala	VPCGK_014	MT217033
23	<i>Cnemaspis anamudiensis</i>	Anamudi RF, Idukki, Kerala	VPCGK_016	MT217034
24	<i>Cnemaspis</i> sp. (Vagamon)	Vagamon, Kerala	VPCGK_021	MT217035
25	<i>Cnemaspis heteropholis</i>	Devarakolli, Madikeri, Karnataka	BNHS 2745	MT217039
26	<i>Cnemaspis kottiyoorensis</i>	Devarakolli, Madikeri, Karnataka	BNHS 2747	MT217038
27	<i>Cnemaspis kottiyoorensis</i>	Paithalmala, Kannur, Kerala	VPCGK_052	MT217037*
28	<i>Cnemaspis palakkadensis</i> sp. nov.	Anakkal, Palakkad, Kerala	BNHS 2790	MT762366
		Outgroups		
29	<i>Phelsuma lineata</i>	Madagascar	ZCMV_2029	KC438463
30	<i>Phelsuma v-nigra</i>	Moheli, Comoros	MH10	FJ829967
31	<i>Phelsuma ornata</i>	Reunion	Sound_P7	DQ270577
32	<i>Lygodactylus picturatus</i>	Tanzania	LYG_4	HQ872462
33	<i>Lygodactylus miops</i>	Madagascar	LUS8	LN998673
34	<i>Lygodactylus madagascariensis</i>	Madagascar	LM1A	LN998665

Appendix 2. Specimens examined.

Cnemaspis aaronbaueri: BNHS 2607, BNHS 2608, and BNHS 2609 (females), from Thenmala, Kollam District, Kerala, India.

Cnemaspis beddomei: collection of the Natural History Museum, London (NHMUK), NHMUK 1946.9.4.83 (male), from South Tinnevelly, Tirunelveli, southern Tamil Nadu State, India.

Cnemaspis gracilis: NHMUK 74.4.29.393 (male), from “Palghat Hills” (Kerala State, India), and BNHS 2513 and BNHS 2514, collected from the Palakkad, Kerala, used for examination and genetic analysis.

Cnemaspis indica: NHMUK 46.11.22.22b (male), BNHS 1252–10 (male), Nilgiris, Tamil Nadu, India.

Cnemaspis kolhapurensis: BNHS 1855 (male), Dajipur, Kolhapur district, Maharashtra; and BNHS 2447 and BNHS 2448, from Amboli, Sindhudurg district, Maharashtra, India.

Cnemaspis kottiyooorensis: BNHS 2519 from Kannur, Kerala state, India.

Cnemaspis littoralis: Neotype ZSI/WGRC/IR/V/2377 (male) from Chaliyam, Kozhikode, Kerala; ZSI/WGRC/IR/V/2378a and ZSI/WGRC/IR/V/2378b (males) from Narayamkulam (= Chengodumala), Kozhikode, Kerala; ZSI/WGRC/IR/V/2379a (male) and ZSI/WGRC/IR/V/2379b (female) from Kapprikad, Ernakulam, Kerala; ZSI/WGRC/IR/V/2380 (male) from Chaliyam, Kozhikode, Kerala; ZSI/WGRC/IR/V/2381a and ZSI/WGRC/IR/V/2381b (males) from Nellikuth, Mallapuram, Kerala; BNHS 1150 (male), from Nilambur, Malabar, Kerala state, India. BNHS 2517 and BNHS 2518 from the Kozhikode, Kerala state, India.

Cnemaspis maculicollis: ZSI/WGRC/IR/V/2704 (male), from Pandimotta, Shendurney Wildlife Sanctuary, Kollam District, Kerala, India.

Cnemaspis nilagirica: NHMUK 74.4.29.729 (female), Nilgiris, Nilgiri District, Tamil Nadu State, south-western India.

Cnemaspis ornata: Lectotype NHMUK 74.4.29.400 (male), paralectotype NHMUK 74.4.29.401 (male), NHMUK 74.4.29.404 (female), NHMUK 74.4.29.405 (female), NHMUK 74.4.29.406 (female), NHMUK 74.4.29.407 (female), NHMUK 74.4.29.408 (female), and NHMUK 74.4.29.409 (female), from South Tinnevelly Hills, Tirunelveli, Tamil Nadu State, India.

Cnemaspis sisparensis: NHMUK 74.4.29.383 (male), from Sholakal, the foot of SisparaGhat, Kerala, India.

Cnemaspis wynadensis: BMNH 74.4.29.355 (male), from Wynad, Kerala, and BNHS 1042, BNHS 1043 (male), Mannarghat, Palghat, Kerala, India.